

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 120365

TO: Vanessa L Ford

Location: rem/3b25/3c18

Art Unit: 1645

Search Notes

Tuesday, April 27, 2004

Case Serial Number: 10620049

From: Barb O'Bryen

Location: Biotech-Chem Library

Remsen 1A69

Phone: 571-272-2518

BUB

barbara.obryen@uspto.gov

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Scoring table:

Searched:

Database :

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Sequence:

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Run on:

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Mis musculus (house mouse)

Mis musculus

Mis musculus

Bukaryota; Metazoa; Chordara; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 616)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabs-remail.ilh.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Prayaration: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

Clone distribution: NCI-CGAP clone distribution information can be http://image.lln.gov

Plate: LiAM9245 row: j column: 04

High quality sequence stop: 613.
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CA578534
BF144339
BF581992
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BG968682
BF582283
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BF138189 601781314
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Copyright (c) 1993 - 2004 Compugen Ltd.
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NIH-MGC http://mgc.nci.nih.gov/.

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Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: GapDa-rémail.nih.gov
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CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be
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Investigator providing samples: Gilbert Smith, NIH"
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                                    organism="Mus musculus"
Socation/Qualifiers
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/strain="Czech II"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
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National Institutes of Health, Mammalian Gene Collection (MGC)
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87.9%; Pred. No. 1.7e-58;
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
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Site_2: Not1; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
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Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Aiba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H. Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9282 row: n column: 06
High quality sequence stop: 649.
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Best Local Similarity 92.2%; Pred. No. 2.1e-58;
Matches 308; Conservative 0; Mismatches 26; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                        1. .669
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Other ESTS: K0731A05-3
Contact: Dawcod B. Dudekula
Laboratory of Genetics
Antional Institute on Aging/National Institutes of Health
N313 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, UI
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0731 row: A column: 05
Seq primar: M13 Reverse
High quality sequence stop: 462
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Gaps . 0 Query Match 38.1%; Score 282; DB 14; Length 462; Best Local Similarity 85.1%; Pred. No. 5.1e-56; Matches 315; Conservative 0; Mismatches 55; Indels Conservative 1895; Matches 1895; Conservative 1895; Matches 1895; Conservative 1895; Matches 1895; Matches

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667 CCTCCAGCACACCTACATGCAGCTCAGCAGCCTGACCTCTGTGGACTCTGCGGGTCTATT

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The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.1 kb. The library was constructed by Yulan Piao (NIA)."

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CDNA Library (Long) Mus musculus CDNA clone NIA:K0702C06
IMAGE:30073757 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 481)
1 abao, Y. Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Aiba, X., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (Lin-, C-Kit-, Sca-1-) cDNA Library (Long)
316 CCTCCAGCACAGCCTACATGCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTACT 375
                                668 TCTGTGCAAGATCGGGGTTGCTACGTTATGCTATGGACTACTGGGGTCAAGGAACCTCAG 727
                                                              376 TCTGTGCAAGAGACTACGGTAGTAGCTATAGGTTTGCTTACTGGGGCCAAGGGACTCTGG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory of Genetics
National Institutes of Health
333 Gassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Bmail: cdna@lgv.c.nia.nih.gov
Plate: K0702 row: C column: 06
Seq primer: M13 Reverse
High quality sequence stop: 481
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
Mus musculus
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 955)

S NIH-Morc http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.inh.gov/.

Email: cgapbs-rémail.inh.gov/.

Tissue Procurement: The Cepko Laboratory

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:

High quality sequence stop: 712.

High quality sequence stop: 712. BQ947728
AGENCOURT_8927146 NCI CGAP_CO24 Mus musculus cDNA clone
IMAGE:6394985 5', mRNA sequence. ô 76 crisaadsiriscentricionadiricascriscascástrissascrisascristas 135 487 547 196 ACTGGGTGAAGGCGAGAGGCCTGGAAAGGGTCTTGAGTGGATTGGACGGGTTTATCCTGGAG 255 548 ATGGAGATTCTAACTACAATGGGAAAATTCGAGGGCAAGGCCATACTGACAGGCAGACAAAT 607 608 CCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGTGGACTCTGCGGTCTATT 667 316 cerecadeacadeeracardeaacreaceadeeracerdacarergadaacrergeggreracr 375 376 rengrecaagaeneraegeragrageraraegeringeringeringeregegeenagegaereeg 435 668 TCTGTGCAAGATCGGGGTTGCTACGTTATGCTATGGACTACGGGGTCAAGGAACCTCAG 727 136 GGGCCTCAGTGGAAGTTTTCCTGCAAGGCTTCTGGCTACGCATTCAGTAGGCTGGATGA 428 GGGCCTCAGTGAAGATTTCCTGCAAAGATTCTGGCTACGCATTCAATAGCTCTTGGATGA 368 CCGGTGGTGGTGGATCCGAGGTCCAACTGCAACAGGTCTGGACCTGAGCTGAAGCCTG 488 ACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGATTGGACGGATTTATCCTGGAG Gaps , 0 38.1%; Score 282; DB 14; Length 481; larity 85.1%; Pred. No. 5.2e-56; Conservative 0; Mismatches 55; Indels /organism="Mus musculus" /mol_type="mRNA" /strain="FVB/N" /db xref="taxon:10090" /clone="IMAGE:6394985" BQ947728.1 GI:22363206 436 TCACTGTCTC 445 728 TCACCGICTC 737 Similarity source VERSION KEYWORDS SOURCE ORGANISM DEFINITION TITLE JOURNAL COMMENT REFERENCE AUTHORS ACCESSION FEATURES

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us-10-620-049-24.rst

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Mus musculus (house mouse)

Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mus musculus

Bukaryota; Matazoa; Chordata; Sciurognathi; Muridae; Murinae; Musc.

Bukaryota; Mac. noi.nih.gov/.

I (bases 1 to 1459)

S NIH-Mor http://mgc.noi.nih.gov/.

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L (contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov/.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov/

Tissue Procurement: The Cepko Laboratory

Tissue Procurement: The Cepko Laboratory

Tissue Procurement: The Cepko Laboratory

Contact: Robert Strayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llh.gov

Plate: LiAM13895 row: c column: 15

High quality sequence start: 165

High quality sequence etart: 165

High quality sequence etart: 165

High quality sequence start: 165
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Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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                                                                                                                                                                                                                                                                                                                                                                                  1459 bp mRNA linear EST AGENCOURT 8885602 NCI CGAP C024 Mus musculus cDNA clone INAGE:6397382 5', mRNA sequence.
BQ918407.1 GI:22333105
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                                                                                                                                                                                                                                                                                   tch 37.9%; Score 281.2; DB 12; Length 827; al Similarity 90.1%; Pred. No. 1e-55; 301; Conservative 0; Mismatches 33; Indels 0;
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/mol_type="mRNA"
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 827)

S NIH-McG http://mgc.nci.nih.gov/

S NIH-McG http://mgc.nci.nih.gov/

L Unpublished (1999)

L Unpublished (1999)

L Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.inih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

Contact: Robert Strayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clond Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clond through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

L column: 04

High quality sequence stops: 827.
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                                                                                                                                                                                                                                                                                                                                     TCTGTGCAAGATCGGGGTTGCTACGTTATGCTATGGACTAGGGGGTCAAGGAACCTCAG 727
       /lab host="DH10B (TI phage-resistant)"
/clone lib="NCI CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/organism="Mus musculus"
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BI152061.1 GI:14612062
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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'strain="FVB/N"
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Best Local Similarity
Matches 301; Conserv
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Divaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 891)

S NIH-MGC http://mgc.nci.nih.gov/.

S NIH-MGC http://mgc.nci.nih.gov/.

L Orpublished (1999)

L Conteat: Robert Strausberg, Ph.D.

Email: cgapbe.r@mail.nih.gov/

Tissue Procurement: Gilbert Smith, Ph.D.

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov

Plate: LLAM9249 row: o_column: 04
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/clone="IMAGE:4023550"
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/mol type="mRNA"
/strain="Czech II"
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Location/Qualifiers
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Best Local Similarity 91.9%;
Matches 307; Conservative
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487 200 547 607 320 667

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/organism="Mus musculus"
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/strain="Czech II"
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Stem cell origin."
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/clone lib="NOI CGAP Lu29"
/note="Organ: lung; Vector: pCMV-spORT6; Site_I: SalI;
Site_2: NOII; Cloned unidirectionally. PrimeT: Oligo dT.
LibTary constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus (house couse)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AK007163 689 bp mRNA linear HTC 20-SEP-2 Mus musculus adult male testis CDNA, RIKEN full-length enriched library, clone:1700110111 product:immunoglobulin heavy chain 6 (heavy_chain of IgM), full insert sequence.
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llarity 84.8%; Pred. No. 1.3e-53;
Conservative 0; Mismatches 51; Indels
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9279253
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319; Conserv
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/db_xref="taxon:10090"
/clone="InAdaE:4011099"
/tissue_type="Lumor, metastatic to mammary"
/lab_host="DH10B"
/lab_host="DH10B"
/clone=lib="NGI CGAP_Lung"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; transgenic model WNT-1, expression driven by WNTV-Irrs enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
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602848859F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5012343 5',
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Mus musculus
Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
I (bases I to 86)
INH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nth.gov
Issue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1063 row: e column: 16
High quality sequence stop: 862.
Location/Qualifiers
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155. - 490 / Anotes condit... / 156. - 490 / Anotes protein product; immunoglobulin heavy chain evidence: BLASIN, 100%, match=137)
                                                                                                                                    f.codon_start=1
/proteIn_id="BAB24877.1"
/db_xref="G1:12840554"
/translation="MTGVHSQVQLQQSGPBLVKPGASVKISCKASGYAFSSSWMNWVK
QRPGXGLBATIOn="MTGVHSQVQLQQSGPBLVRPGASSSTAYMQLSSLTSEDSAVYFC
ARHSVTTTS"
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602889345F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5044690
 clone lib="RIKEN full-length enriched mouse cDNA library"
dev_stage="adult"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
Tona Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
Plate: LiAMIII.2 row: i column: 11
High quality sequence stop: 706.
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Best Local Similarity 92.5%;
Matches 284; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                              The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                      the FANTOM Consortium and the RIKEN Genome Exploration Research
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| Mol type="mRNN"
| strain="C57BL/6J"
| db_xref="MG1.910224"
| db_xref="MG1.910224"
| db_xref="mG1.1910224"
| db_xref="taxon:10090"
Genome Res. 10 (10), 1617-1630 (2000)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. B. (bases 1 to 417)

E. (bases 1 to 417)

S. Margul, G. J., Dudekula, D. B., Qian, Y., Luo, A., Carter, M. G., Aiba, K., Taub, D., Longo, D. L., Keller, J. and Ko, M. S. H.

Systematic Analyses of NIA Mouse Hematopoietic Stem Cell

(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)

L. Unpublished (2001)

L. Unpublished (2001)

Cother ESTS: KOT10F01-3

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Emal: cdna@lgeun.grc.nia.nih.gov

Plate: KOT10 row: F. Column: 01
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stem cell origin."
/lab host="hullo"
/clone lib="NUL CGAP Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
/note: lung; Vector: pCMV-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 TCTGTGCAAGA---CGGCGGGACCCAACTACTTGACTACTGGGGCCAAGGCACCACTA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 GGGCCTCAGTGAAGATTTCCTGCAAAGCTTCTGGCTACGCATTCAGTAGCTCCTGGATGA 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGTGGACTCTGCGGTCTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.2%; Score 268.2; DB 10;
llarity 86.1%; Pred. No. 1.3e-52;
Conservative 0; Mismatches 48;
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Mus musculus
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CA577519.1 GI:25125910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCACAGTCTCCTC 420
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Matches 321;
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Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Musmmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 940)

2 NIH-MGC http://mgc.nci.nlh.gov/.

In (bases 1 to 940)

In (base 2 to 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 940 bp mRNA linear EST 30-OCT-2000 G01775295F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017214 5', mENA sequence.
BF169023
BF169023.1 GI:11049375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Sali; cloned undirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGAACTGTTAAACTCCTAATTACACATCAAGATTACACTCAGGAGTCCCATCAA 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.3%; Score 269; DB 12;
88.0%; Pred. No. 7.2e-53;
iive 0; Mismatches 40;
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/mol_type="mRNA"
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                                                                                                                                        /tissue_type="Hematopoietic Stem Cell
(Lin-/G-Kit-/Sca-1-)"
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High quality sequence stop: 417
POLYA=No.
                          Location/Qualifiers
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Search completed: April 26, 2004, 17:37:51 Job time : 2550 secs

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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

April 26, 2004, 15:43:02; Search time 393 Seconds (without alignments) 8009.961 Million cell updates/sec Run on:

US-10-620-049-24 741

1 gatattcagatgacacagac..........cctcagtcaccgtctcctcg 741 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3373863 segs, 2124099041 residues Searched: 6747726 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequ1990s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

	Descr	AAA58773 Aaa58773 DNA encod	ABK13467 Abk13467 DNA encod	_	ABK13464 DNA encod		ADD25786 Add25786 Binding d			ACF05482 Anti-CD7	ACF05481 Anti-CD7	AAA39167 Apoptobod	AAD35252 Murine CC	Aaz43431	ACC79606 Acc79606 Plasmid p		Abk89855	ADD25448 ADD25448 Binding d	AAZ88358 AAZ88358 Bispecifi		AAT94967 Aat94967 R. pipien	AAT94965 R. pipien	AAT94968 R. pipien	CONTRACTOR OF CO
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ALIGNMENTS

Immunotoxin, CD3-binding domain; Pseudomonas exotoxin A; immune system; scFv(UCHT-1)-PE28; T-cell mediated disease; transplant rejection; host versus graft disease; graft versus host disease; bone marrow transplant; ss. DNA encoding an immunotoxin comprising a CD3 binding domain and PE28. AAA58773 standard; DNA; 1803 BP. 99US-00232445. 99US-00236968. 99US-00414134. 13-JAN-2000; 2000WO-EP000245. (first entry) Mus sp. Pseudomonas aeruginosa. 15-JAN-1999; 25-JAN-1999; 07-OCT-1999; WO200041474-A2 20-0CT-2000 20-JUL-2000. Synthetic. AAA58773; RESULT 1 AAA587

(NOVS) NOVARTIS AG. (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

Digan ME, Lake P, Wright RM; WPI; 2000-482739/42.

P-PSDB; AAB07461.

Recombinant immunotoxin used for prophylaxis and treatment of $\mathtt{T-cell}$ mediated diseases e.g. transplantation rejection.

Disclosure; Page 55-59; 75pp; English.

The present sequence encodes a recombinant immunotoxin comprising a CD3-binding domain and a Pseudomonas exotoxin A component. It is designated scFv(UCHT-1)-PE28. The immunotoxins of the invention are used for the prophylaxis or treatment of T-cell mediated diseases or conditions of the

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immune system. They are also used to condition a patient to be transplanted with cells, or a tissue or an organ of a donor and for the prophylaxis and/or treatment of acute or chronic transplantation rejection, host versus graft disease and/or graft versus host disease in a patient to undergo a bone marrow transplant, where the CD3-bearing cell population in the patient is depleted and an inoculum comprising isolated bone marrow and/or stem-cell enriched peripheral blood cells of the donor treated with immunotoxin is inoculated into the patient
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The invention relates to an anti-T cell immunotoxin fusion protein, comprising from the amino terminus, a truncated diphtheria toxin moiety, a connector, and one single chain FV comprises VL, L, or VH, L is a Gly-Ser inches, and VL and one single chain FV comprises VL, L, or VH, L is a Gly-Ser inches, and VL and VH are the variable light and heavy domains of the anti-Dody uffrit. Also included are a uncleic acid encoding the novel immunotoxin fusion protein, a vector comprising the nucleic acid novel immunotoxin fusion protein, a vector comprising the nucleic acid and a cell comprising the nucleic acid. The immunotoxin may also be a pseudocomas endocoxin A (ETA). The immunotoxin fusion proteins are useful for treating T cell leukaemis or lymphomas, graft-versus-host diseases, and autoimmune to greave to propulations of T cells, or exvivo to effect T-cell depletion from a treated cell population. The fusion proteins can be administered to a subject who is or will be a cepient of an allotransplant to prevent or reduce T-cell mediated corbinates or organ in the subject as well as treat other T-cell mediated ciseases such as systemic lupus erythematosus, type I diabetes, the intermediated arrefered to the transplant of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious diseases of the immune system (e.g. AIDS (acquired immunodeficiency syndrome)) and chronic immunosuppression. The present sequence encodes an immunotoxin fusion protein of the invention comprising 389 residues from the N-terminal glycine of mature DT toxin, a (Gly4Ser) 3 linker and one single Fv chain from antibody UCHTI, DT389.sFv(UCHTI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New anti-T cell immunotoxin fusion protein comprising a truncated diphtheria toxin moiety, a connector, and one single chain Fv of the variable region of a UCHT1 antibody, useful for treating e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MI
(USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 34; Fig 35; 307pp; English
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RESULT 2
ABK13467
ID ABK1
XX
AC ABK1
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ABK13467 standard; DNA; 1943 BP

ABK13467

Digan ME;

Hexham JM,

Ma S,

Woo J,

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cytostatic; imminosuppressive; imminostimulant; antidiabetic; antirheumatic; antiarthritic; anti-HIV; anti-inflammatory; antirheumatic; antiarthritic; anti-HIV; anti-inflammatory; anti-r cell immunocxin fusion protein; antibody; UCHII; (Gly49er) 3 linker; T cell leukaemia; lymphoma; gene; ds; graft-versus-host disease; FV; autoimmune disease; transplant rejectis systemic lupus erythematoeus; type i diabetes; rheumatoid arthritis; angasthenia gravis; multiple sclerosis; AIDS; DT389.seV(UCHII); acquired immunodeficiency syndrome; chronic immunosuppression.
                                                                                                                                                  diphtheria toxin,
                                                                   DNA encoding Immunotoxin fusion protein DT389.sFv(UCHT1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product= "DT389.sFv(UCHT1)"
                                                                                                                                              Immunotoxin; pseudomonas exotoxin A; ETA;
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3. 1932
/*tag= a
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Synthetio.
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23-APR-2002
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Example 1; Fig 15; 58pp; English.
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                                                                                                                  Gaps
                                                                                                                  18;
                                                                      Length 1943;
                     Seguence 1943 BP; 571 A; 395 C; 485 G; 492 T; 0 U; 0 Other;
                                                                 Score 499.4; DB 6; Length
Pred. No. 1.1e-120;
0; Mismatches 121; Indels
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                                                                                         Best Local Similarity 81.4%;
Matches 610; Conservative
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Recombinant immunotoxin; scFV(UCHT-1)-PE38; single chain Fv fragment; murine; anti-human CD3-monoclonal antibody binding domain; UCHT-1; Pseudomonas aeruginosa; exotoxin A; ADP-ribosylating; translocation; recombinant immunotoxin, scFv(UCHT-1)-PE38. ABX14413 standard; DNA; 1944 BP. (first entry) DNA encoding 06-MAR-2003 ABX14413; RESULT

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T-cell mediated disorder; organ transplantation rejection; autoimmune disease; graft versus host disease; bone marrow transplant; acquired immunodeficiency syndrome; AIDS; T-cell leukaemia; T-cell lymphoma; T-cell-mediated autoimmune disease; type I diabetes; systemic lupus erythematosus; Theumatoid arthritis, myasthemia gravis; multiple solerosis; immunological tolerance; osteoporosis; aplastic anaemia; Gaucher's disease; thalassaemia; mutant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel recombinant immunotoxin polypeptide useful for treatment or prophylaxis of T-cell mediated disorders or organ transplantation rejection, comprises a CD3-binding domain and a Pseudomonas exotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "scFv (UCHT-1) -PE38"
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/*tag= a
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                                                                                                                                                                                                                                                             Mus sp.
Pseudomonas aeruginosa
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P-PSDB; ABG72265.
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(LAKE/) LAKE P.
(WRIG/) WRIGHT R M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2002142000-A1.
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                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                         Chimeric.
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The present invention relates to a novel recombinant immunotoxin, scrV(UCHT-1)-PE38, and the polynucleotide sequence encoding it. The recombinant immunotoxin comprising a single chain (sc) Pv fragment of murine anti-human CD3-monoclonal antibody (UCHT-1) binding domain fused communication comprising a single chain (sc) Pv fragment of murine anti-human CD3-monoclonal antibody (UCHT-1) binding domain fused consideration and translocation functions but substantially diminished consideration or prophylaxis of T-cell mediated disorders, organ transplantation rejection or autoimmune disease in a patient. For example, scPv(UCHT-1)-PE38 may be used for treatment or prophylaxis of transplant, for the treatment or prophylaxis of transplant rejection in a patient to undergo a bone marrow transplant, for the treatment or prophylaxis of transplant rejection in a patient to be transplanted with cells, tissue or organ of a donor.

CC patient to be transplanted with cells, tissue or organ of a donor.

CC scPv(UCHT-1)-PE38 is also useful for treating acquired immunodeficiency conditioning a cutoimmune disease such as systemic lupus erythemacosus, type I diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis, for inducing immunological tolerance, and for treating diseases cutable or treatable condition marrow transplantation, including leukaemias, osteoporosis, aplastic anaemia, daucher's disease, and thalassaemia. The present condition immunotoxin, scfv(UCHT-1)-PE38

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18; DB 7; Length 1944; Sequence 1944 BP; 389 A; 623 C; 605 G; 327 T; 0 U; 0 Other; Query Match 67.4%; Score 499.4; DB 7; Length 1 Best Local Similarity 81.4%; Pred. No. 1.1e-120; Matches 610; Conservative 0; Mismatches 121; Indels

9 1 GATATTCAGATGACACAGACTACATCCTCCCGGCTCTCTGGGAGACAGAGTCACC

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WO200187982-A2

Synthetic Chimeric.

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                                             69 AICAGTIGCAGGCAAGICAGGACATIAGAAAITAITIAAACTGGTATCAACAGAAACCA
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Immunotoxin, pseudomonas exotoxin A, ETA, diphtheria toxin, DT, cytostatic; immunosuppressive, immunostimulant; antidiabetic; antidibumatic; antidibumatic; imflammatory; anti-inflammatory; anti-inflammatory; anti-inflammatory; T cell immunotoxin fusion protein; antibody; UCHT1, T cell leukaemia, lymphoma, AIDS, graft-versus-host disease; Frisusplant rejection, systemic lupus erythematosus; type I diabetes; rheumatoid arthritis; myasthenia gravis; multiple sclerosis, sp. (ald)dmDT390-bisFv(UCHT1*); acquired immunodeficiency syndrome; chronic immunosuppression; ds.
                                                                                                                                                  encoding immunotoxin fusion protein sp-(ala)dmDT390-bisFv(UCHT1*)
                                  ABK13464 standard; DNA; 2952 BP
                                                                                                                                                                                                                                                                                                                                                                                   Mus sp.
Corynebacterium diphtheriae
                                                                                                               (first entry)
                                                                                                               23-APR-2002
                                                                           ABK13464;
                                                                                                                                                      DNA
                  RESULT 4
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The invention relates to an anti-T cell immunotoxin fusion protein, comprising from the amino terminus, a truncated diphtheria toxin molety, a connector, and one single chain by of the variable region of a UCHT1 antibody. The single chain by of the variable region of a UCHT1 clinker, and VL and VH are the variable light and heavy domains of the intibody. The single chain by contribed are a nucleic acid encoding the novel immunotoxin fusion protein, a vector comprising the nucleic acid monors endotoxin A (BTA). The immunotoxin may also be a pseudomonas endotoxin A (BTA). The immunotoxin may also be a pseudomonas endotoxin A (BTA). The immunotoxin may also be a cell leukaemis or lymphomas, graft-vergus-host diseases, and autoimmune diseases by inducing immune tolerance. The immunotoxin fusion proteins may be used in vivo to systemically reduce populations of T cells, or exvivo to effect T-cell depletion from a treated cell population. The fusion proteins can be administered to a subject who is or will be a recipient of an allotrangplant to prevent or reduce T-cell mediated acute or organ in the subject as well as treat other T-cell mediated che remained of a systemic lupus erythematosus, type I diabetes, infectious diseases of the immune system (e.g. AlDS (acquired immunodeficiency syndrome)) and chronic immunosuppression. The present sequence encodes an
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                                                                                                                                                                                                                                                                                                                                                                      New anti-T cell immunotoxin fusion protein comprising a truncated diphtheria toxin moiety, a connector, and one single chain Fv of the variable region of a UCHII antibody, useful for treating e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GAAGATATTGGCACTTACTTTTGCCAACAGGGCAATACGCCTCCGTGGACGTTCGGTGGA
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                           Neville DM, Thompson JT, Hu H, Woo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 89; Page 278-279; 307pp; English.
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Best Local Similarity 80.2%;
Matches 587; Conservative
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                                                                                                                                                                          .8-MAY-2000; 2000US-00573797
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/note= "L6 light chain variable region leader"
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/note= "encodes helical peptide linker"
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Pred. No. 1.7e-115;
0; Mismatches 148; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 913 BP; 252 A; 223 C; 228 G; 210 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                    Linsley PS,
                                                                                                                                                                                                                                                                                                                    Hayden MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 11; 50pp; English.
                                                                                                                                                                                         (BRIM ) BRISTOL-MYERS SQUIBE CO
93US-00013420.
93US-00121054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.7%;
                                                                                                                                                                                                                                                                                                             Gilliland LK,
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Matches 581; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis and treatment.
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300 375 360 435 420 492

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121 GACGGAACTGTTAAATTCCTGATCTACTACATCAAGATTACTGCCAGGAGTCCCATCA 180
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                                                                                                                                                                                                                                                                                                    GGCACCAAGCTGGAAATAAAACGTGGTGGAGGTGGTTCTGATGGTGGTGGTTCTGGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        667 GACAAGTCATCCAGCACAGCCTACATGGAGCTCCTCAGTCTGACATCTGAAGACTTCTGCA
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                                                                                                           181 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCCCTCACCATTAACAACCTGGAGCAG
                                                                                                                                                     AGGITCAGTGGCAGTGTGGAACAGATTATTCTCTCACCATTGCCAACCTGCAACCA
                                                                                                                                                                                                                                     GAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTGGACGTTCGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                           436 GGTGG----CGCCGGATCTATCGATGAGGTCCAGCTGCAACAGTCTGGACCTGAACTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCCTGGGGCCTCAGTGAAGATTTCCTGCAAAGATTCTGGCTACGCATTCAATAGCTCT
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                                                      GATGGAACTGTTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA
                                                                                                                                                                                                                                                                                                                                              <u>escaccada acristra accada actesta se concesta escontes actes acte</u>
                                                                                                                                                                                                                                                                                                                                                                                              GCCGCCTCCGGTGGTGGTCCAACTCCAACTGCAACAGTCTGGACCTGAGCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  493 AAGCCTGGAGCTTCAATG----TCCTGCAAGGCCTCTGGTTACTCATTCACTGGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 TGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGATTGGACGGATTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            547 ATCGTGAACTGGCTGAAGCAGAGCCATGGAAAGAACCTTGAGTGGATTGGACTTATTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 CCTGGAGATGGAGATTCTAACTACAATGGGAAATTCGAGGGCAAGGCCATACTGACAGCA
                                                                                                                                                                                                          GAAGATATTGGCACTTACTTTTGCCAACAGGGCAATACGCCTCCGTGGACGTTCGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding anti-CD3 scFv for gene therapy of cancer.
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7. .1674
/*tag= a
/product= "Anti-CD3 a
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds, Binding domain, immunoglobulin, fusion protein, cytostatic, antiarthritic, immunosuppressive, antidiabetic; antithyroid, neuroprotective, hinge region; immunoglobulin heavy chain; CH2 constant region, CH3 constant region, IgG1, antibody dependent cell-mediated cytotoxicity, ADCC; complement fixation, antigonat condition, B-cell disorder; melanoma; carchinoma; sarcoma; rheumatoid arthritis, myaethenia gravis, Grave's disease, type I diabetes mellitus; multiple sclerosis; autoimmune disease.
672
                                                                                       732
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                                                                                                                                                                                 733 Grenarhacherecaagarenegenaenangareacheenegrachernegareneer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GTCAGTTGCAGGCCAAGTCAGGACATTAGGAATTATTTAAACTGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GATATICAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC
CCATACAAAGGTCTTACTACCTACAACCAGAAATTCAAGGGCAAGGCCACATTAACTGTA
                                               GACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGTGGACTCTGCG
                                                                                       673 GACAAGTCATCCAGCACAGCCTACATGGAGCTCCTCAGTCTGACATCTGAAGACTCTGCA
                                                                                                                                      GTCTATTTCTGTGCAAGATCGGGGTTGCTACGTTATGCTATGGACTACTGGGGTCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Binding domain-immunoglobulin fusion protein-associated DNA #188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 463.8; DB 9;
Pred. No. 2.1e-111;
0; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thompson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ledbetter JA, Hayden-Ledbetter MS,
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17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.6%;
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                                                                                                                                                                                                                                721 ACCTCAGTCACC 732
                                                                                                                                                                                                                                                                                  793 GGCGCAGGGACC 804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-801317/75.
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Matches 594;
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727 GTCTATTACTGTGCAAGATCTGGGTACTATGGTGACTCGGACTGGTACTTCGATGTCTGG 786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an anti-T cell immunotoxin fusion protein, comprising from the amino terminus, a truncated diphtheria toxin moiety, a connector, and one single chain Fv of the variable region of a UCHTI antibody. The single chain Fv comprises VV, L, or VH, L is a Gly-Ser linker, and VL and VH are the variable light and heavy domains of the anti-CD3 antibody UCHTI. Also included are a nucleic acid encoding the
                                                                                                                                                                            GACAAGECATCCAGCACACACCTACATGGAGCTCCTCAGTCTCACATCTGAAGACTCTGCA
547 ATCGTGAACTGGCTGAAGCAGAGCCATGGAAAGAACCTTGAGTGGATTGGACTTATTAAT
                                             CCTGGAGATGGAGATTCTAACTACAATGGGAAATTCGAGGGCAAGGCCATACTGACAGCA
                                                                                                                                        GACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGTGGACTCTGCGC
                                                                                                                                                                                                                                   GICTATITICIGIGCAAGAICGGGTIGCTACGTIAIGC-----TAIGGACTACIGG
                                                                                      ccatacaaaggrettactacctacaaccagaaattcaagggccaaggccacattaactgta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunotoxin, pseudomonas exotoxin A, ETA, diphtheria toxin, DT cytostatic; immunosuppressive; immunostimulant; antidiabetic; antistrheumatic; antiarthritic; anti-HT, anti-Inflammatory; anti-Trecall immunotoxin (usion protein; antibody, UCHT1; (Gly4Ser)3 linker, T cell leukaemia; lymphoma; gene; ds; graft-versus-host disease; Fv; autoimmune disease; transplant systemic lupus erythematosus; type I diabetes; rheumatoid arth myasthenia gravis; multiple sclerosis; AIDS; acquired immunodeficiency syndrome; chronic immunosuppression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hexham JM,
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                                                                                                                                                                                                                                                                                                                                                                    GCGCAGGACCACGTCACCGTCTCTC 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding an Immunotoxin fusion protein.
                                                                                                                                                                                                                                                                                                                                   GGTCAAGGAACCTCAGTCACCGTCTCCTC 740
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES ME
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 91; Page 300-301; 307pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK13612 standard; DNA; 2691
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-121980/16.
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ABK13612
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                                                                                                                                                                                                                                                                                                                                                                         The present sequence is of a DNA construct encoding a mouse-human CD3 chimeric single chain (sc) FV comprising the G19-4 mouse anti-human CD3 VL domain joined via a peptide linker to HG19-4 mouse anti-human CD3 VL domain joined via a peptide linker to HG19-4 mouse anti-human CD3 VL domain, human IgG1 FC domain (hinge, CH2, CH3) and human CD80 VH domain, human in the CD80 VH domain in the VRappa of transmembrane and cytoplasmic domains, with an N-terminal LG VRappa leader peptide. The coding sequence was constructed to provide expression of active anti-CD3 monoclonal antibody scPv at the tumour cell surface. The DNA construct, or a cell transfected with it, can be used for in vivo cancer therapy. It is believed that the anti-CD3 scPv expression on the surface of tumour cells induces polyclonal T cell activation and tumour cell destruction, relaesing tumour antigens and promoting a transition to antigen-specific tumour immunity, detected as rejection of 'wild-type' (not transfected) cells from the same tumour. In an example from the inverse polyclonal stimulation of T cells to proliferate, produce Thi type lymphokines, to become cytolytic and to have antitumour activity in vivo.
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                                                                                                                                                                                                                                   New culture system for generating tumor-reactive T-lymphocytes comprises T-cells from a cancer patient, antigen-presenting cells, autologous or allogeneic tumor cells, and immobilized antibodies to T-cell receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 ATCAGTIGCAGGGCAAGTCAGGACATICGCAATTATTIAAACTGGTATCAGCAGAAACCA
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                                                                                                                    Hellstrom KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 463.8; DB 9; Length 1687;
Pred. No. 2.2e-111;
0; Mismatches 137; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1687 BP; 434 A; 470 C; 431 G; 352 T; 0 U; 0 Other;
                                                                                                                 Hayden-Ledbetter M,
                                                                                                                                                                                                                                                                                                                                   Example 2; SEQ ID NO 1; 112pp; English.
                           26-MAR-2002; 2002US-00107991
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al Similarity 79.3%;
594; Conservative (
                                                                                                                      'n,
                                                                                                                 Hellstrom
                                                                    (GENE-) GENECRAFT INC.
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Best Local Similarity
Matches 594; Conserval
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P-PSDB; ADE86039.
                                                                                                                      Ledbetter JA,
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cc novel immunotoxin fusion protein, a vector comprising the nucleic acid and a cell comprising the nucleic acid. The immunotoxin may also be a pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T cell leukaemias or lymphomas, graft-versus-host diseases, and autoimmune diseases by inducing immune tolerance. The immunotoxin fusion proteins may be used in vivo to systemically reduce populations of T cells, or extrain proteins can be administered to a subject who is or will be a recipient of an allotrangplant to prevent or reduce T-cell mediated acute or chronic transplant rejection of the transplanted allogenet cells, tissue or organ in the subject as well as treat other T-cell mediated diseases such as systemic lupus erythematosus, type I diabetes, or cheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious diseases of the immune system (e.g. AIDS (acquired immunodeficiency syndrome)) and chronic immunosuppression. The present sequence encodes and the N-terminal glycine of mature DT toxin, a (Gly45er) 3 linker and one single Fv chain from antibody UCHI, and has had its AT content altered to enable expression in yeast
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                                                                                                   GACAAGTCATCCAGCACAGCCTACATGGAACTCCTCAGTCTGACACTCTGAGGACTCTGCA
                                                                              1 GATATTCAGATGACACAGACTACATCCTCCTGTCTGCCTCTCTGGGAGACAGAGTCACC
                                                                                                                                                                                                                                                                                             181 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCCCTCACCATTAACAACCTGGAGCAG
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                                                                                                                                                  61 GTCAGTTGCAGGCCAAGTCAGGACATTAGGAATTATTTAAACTGGTATCAGCAGAAACCA
                                         27; Gaps
 58.3%; Score 431.8; DB 6; Length 2691; 76.1%; Pred. No. 6.1e-103; tive 0; Mismatches 152; Indels 27;
Query Match
Best Local Similarity 76.1<sup>5</sup>
Matches 570; Conservative
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The present sequence encodes a novel fusion protein comprising an ScFv fragment of anti-CD7 monoclonal antibody TH-69 and domains II and III of Pseudomonas excoxin A (ETA), joined via a peptide linker, and including an N-terminal GHIS tag and C-terminal KDEL sequence. This novel fusion protein binds to CD7-positive T-lymphoid cells and kills them by the indication of apoptosis: It is an example of anti-CD7 serv immunotoxin fusion proteins of the invention. An expression vector, host cells, a method for producing the fusion protein, and a vaccine comprising the cast fusion protein are claimed. The fusion protein is used in the treatment of disorders involved a hyperproliferation of CD7-positive cells, cespecially acute T-cell and/or myeloid leukaemia, and also in the conditioning an animal (e.g. a human) to be transplanted with donor cells, tissue or organ comprises: (a) depleting the CD7-bearing cell conduction in the animal; (b) providing a transplant comprising isolated bone marrow and/or stem cell-enriched peripheral blood cells of the control of the transplant comprising effective amount of the fusion protein or therapeutic composition comprising the fusion protein, and (c) introducing the transplant into the animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fusion protein comprising functionally linked components of an anti-
CD7 antibody or its fragment and an immunotoxin, useful for treating CD7
positive acute T-cell and/or myeloid leukemias, or Graft-versus-host
                                                                                                                                                                                                                               Anti-CD7 antibody TH-69 scPv-Pseudomonas exotoxin A fusion sequence.
                                                                                                                                                                                                                                                            CD7; antibody; TH-69; acFv; exotoxin A; immunotoxin; cytostatic; immunosuppressive; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "TH-69 scFv-ETA fusion protein"
/note= "No start codon"
                 1882 GGTGCTGGTACTACTGTCACTGTCCTC 1910
712 GGTCAAGGAACCTCAGTCACCGTCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 10-11; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .1953
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                                                                                                                         ACF05482 standard; cDNA; 1953
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/product=
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag= a
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P-PSDB; ABR62591.
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                                                                                                                                                                                                                                                                                                                                        Pseudomonas sp.
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                                                                                                                                                                                             06-NOV-2003
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Chimeric.
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                                                                                   RESULT 9
ACF05482
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scFv-ETA fusion protein" codon"

Location/Qualifiers

Mus sp. Pseudomonas sp.

Synthetic. Chimeric.

1. 1956 /*tag= a /partial /product= "TH-69 B /note= "No start c

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                             Seguence 1953 BP; 353 A; 614 C; 655 G; 331 T; 0 U; 0 Other;
                                                                                      Score 421; DB 8; Length 19
Pred. No. 3.7e-100;
0; Mismatches 180; Indels
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Best Local Similarity
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New fusion protein comprising functionally linked components of an anti-CD7 antibody or its fragment and an immunotoxin, useful for treating CD7 positive acute T-cell and/or myeloid leukemias, or Graft-versus-host disease.

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Fey GHM, Gramatzki WPI; 2003-523519/49.

P-PSDB; ABR62590.

(UYER-) UNIV ERLANGEN-NUERNBERG.

14-DEC-2001; 2001US-0339422P.

2002WO-EP014064.

11-DEC-2002; 26-JUN-2003

WO2003051926-A2

Claim 11; Page 10; 55pp; English

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The present sequence encodes a novel fusion protein comprising an scPv fragment of anti-CD7 monoclonal antibody TH-69 and domains III of Pseudomonas exotoxin A (ETA), joined via a peptide linker, and including an N-terminal & EXHs tag and C-terminal REDIK sequence. This novel fusion protein binds to CD7-positive T-1ymphoid cells and kills them by the induction of apoptosis. It is an expression vector, host cells, a check of or producing the fusion protein, and a vaccine comprising the fusion protein are claimed. The fusion protein are claimed. The fusion protein is used in the treatment of disorders involved a hyperproliferation of CD7-positive cells, cepscially acute T-cell and/or myeloid leukaemia, and also in the creatment or prophylaxis of Graft-versue-host disease. A claimed method of conditioning an animal (e.g. a human) to be transplanted with donor cells, itsue or organ comprises: (a) depleting the CD7-bearing cell copulation in the animal, (b) providing a transplant comprising isolated bone marrow and/or stem cell-enriched peripheral blood cells of the transplant of the transplant contor, where the CD7-bearing cell population in (a) and/or the transplant cin (b) are treated with a T-cell depleting effective amount of the fusion protein, and (c) protein or the reappeutic comprising the CD7-pering comprising the CD7
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Anti-CD7 antibody TH-69 scFv-Pseudomonas exotoxin A fusion sequence CD7; antibody; TH-69; scFv; exotoxin A; immunotoxin; cytostatic; immunosuppressive; vaccine; gene; ss.

(first entry)

06-NOV-2003 ACF05481;

ВP

ACF05481 standard; cDNA; 1956

RESULT 10

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WPI; 2000-332086/29.
P-PSDB; AAY91026.
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(HAGI/) HAGIWARA H.
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                                                                                                                                    The present invention describes a method for causing apoptosis in which a fused gene consisting of a gene participating to apoptosis and a gene encoding at least the variable region of anti-idotype antibody is transfected to a cell to express the fused gene and then an idiotype antibody is reacted with the expressed cell. The method is useful in medical, pharmacological and biochemical fields. The present sequence encodes a fusion protein designated apoptobody3sc, which is used in the exemplification of the present invention
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Causing apoptosis comprises transfecting fused gene to cell and reacting cell with idiotypic antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 56.5%; Score 418.6; DB 3; Best Local Similarity 73.6%; Pred. No. 1.5e-99; Matches 554; Conservative 0; Mismatches 184;
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                                                                                            Disclosure; Page 7; 10pp; Japanese.
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Seguence 1545 BP; 403 A; 373 C; 404 G; 365 T; 0 U; 0 Other;

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The invention relates to the use of an antibody and/or chemokine construct that binds a chemokine receptor for preparing a pharmaceutical composition for eliminating cells latently infected with a primate immunodeficiency virus (e.g. human immunodeficiency virus (HTV-1). They are used in gene therapy and as vaccines. The antibody and/or chemokine construct is also used for preparing a pharmaceutical composition for treating, preventing and/or alleviating immunological disorders including autoimmune diseases (e.g. multiple sclerosis, type I diabetes and rhelamation, atopic dermatitis diseases, skin diseases (e.g. skin inflammation, atopic dermatitis and psoriasis), inflammatory diseases such as inflammatory joint diseases (chronic arthritis), inflammatory crenal diseases and graft versus host and transplant rejections. The present sequence is CCREXCD3 bispecific single chain antibody DNA construct. This antibody construct comprises light chain variable domain (VL) and heavy chain variable (VH) domains of mantibody specific for a CD3 antigen joined by a peptide linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of an antibody and/or chemokine construct that binds to a chemokine receptor, for eliminating cells latently infected with primate immunodeficiency virus, or treating, preventing and alleviating immune
                                                                                                                                                                                                                             Chemokine construct; human immunodeficiency virus 1; allergic disease;
                                                                                                                                                                                                                                            skin disease; immunological disorder; autoimmune disease; psoriasis; multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease; diabbetes; skin inflammation; atopic dermatitis; inflammatory disease; inflammatory renal disease; Huv-1; transplant rejection; CGR5xCD3; antibody; chemokine receptor 5; CD3 antigen; chimeric; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a /*tag= horoduct= "CCR5xCD3 bispecific single chain antibody
                                                                                                                                                                                         Murine CCR5xCD3 bispecific single chain antibody DNA construct.
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787 TACTGGGGTCAAGGAACCTCAGTCACCGGATCC
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05-SEP-2001; 2001US-00948004
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P-PSDB; AAE22193.
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                                 Gaps
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                                 18;
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Score 406; DB 6; L
Pred. No. 3e-96;
0; Mismatches 180;
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                                                                                                                                                                                                                                              at least four variable domains that are connected to one another by 1, 2 and 3 peptide linkers. The construct has antivital, antibacterial and cytostatic activity. The multivalent Fv-antibody constructs are useful for the diagnosis and/or therapy of disease, sepecially viral, bacterial or tumor diseases. The multivalent Fv-antibody constructs have increased atability when in the form of a single chain dimer. This sequence encodes a bivalent Fv antibody construct composed of the antibody 9E10 epitope in expression plasmid pDISC3x19-LL
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                                                                                                                                                                              Multivalent Fv-antibody constructs with at least four variable domains connected by 1, 2 and 3 peptide linkers.
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                                                                                                                                                                                                                                                                                                                                                                   Length 1698;
                                                                                                                                                                                                                                                                                                                                            Sequence 1698 BP; 433 A; 434 C; 450 G; 381 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                    Fv-antibody
                                                                                                                                                                                                                                                                                                                                                                 54.5%; Score 404.2; DB 3;
llarity 73.5%; Pred. No. 9e-96;
Conservative 0; Mismatches 163;
                                                                                                                                                                                                                                     multivalent
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                                                                                                       (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                     invention describes a novel
                                                                                                                                                                                                                 Example 1; Fig 5; 14pp; German
                                                              98DE-01019846
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                                                                                                                                                2000-024472/03
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es 577, Conserv
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(a) monomers comprising at least 4 variable domains of which two neighbouring domains of encomer form an antigen-binding VH-VL or VL-VH scFv unit; and/or (b) at least 2 variable domains of a monomer that are non-covalently bound to 2 variable domains of another monomer resulting in the formation of at least 2 additional antigen binding sites to form multimerisation motif. Also described is a process for the preparation of (I) comprising ligating DNA sequences encoding the peptide
                                                                 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multimeric single chain tandem Fv-antibody; antibacterial; virucide; cytostatic; cytokine antegoniet; diagnosis; viral disease; prion disease; bacterial disease; tumoural disease; agglutination; red blood cell; immune system; tumour cell; cytokine; cytotoxic; gene; ds.
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                                                                                                                                                                                                                                                                                                     681
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CAGGGTCTTGAGTGGATTGGACGGATTTATCCTGGAGATGGAGATTCTAACTACAATGGG
                                                                     1018 cagegretrgagregarregacagarrigeceregagargergaracraacracaarega
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/product= "Plasmid pSKK2 scFv3~Li-Db19 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pSKK2 scFv3-LL-Db19 nucleotide sequence.
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P-PSDB; ABR57058.
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linkers with the DNA sequences encoding the variable domains such that the peptide linkers connect the variable domains resulting in the formation of a DNA sequence encoding a monomer of the multivalent multimeric Pv-antibody, and expressing the DNA sequences encoding the various monomers in an expression system. (I) has antibacterial, virucide and cytostatic activities, and can be used as a cytokine antagonist. The multimeric Pv-antibody is useful for diagnosis. The antibody can also be used for the preparation of a pharmaceutical composition for the treatment of a viral, bacterial, lumoural or prion disease, the agglutination of red blood cells, linking cytocoxic cells of the immune system to tumour cells, or linking activating cytokines, cytocoxic substances or a protease to a target cell. The present sequence represents the plasmid pSKMZ serva-LL-DD19 nucleotide sequence, which is used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 395.8; DB 7; Length 1
Pred. No. 1.5e-93;
0; Mismatches 172; Indels
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al Similarity 73.1%;
565; Conservative
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Best Local S:
Matches 565
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The present sequence encodes a bscCD19xCD3 antibody. This antibody is a bispecific single-chain polypeptide comprising domains providing bindingsite of immunoglobulin chains or antibodies specifically recognizing CD19 and CD3 antigen. The polypeptide destroys CD19-positive target cells without any need of T-cell pre and/or co-stimulation, by recruiting cytotoxic T-lymphocytes and so specific lysis by T-cells rather than a polypeptides, or nucleotides encoding them, are used for the treatment of B-cell malignancies, B-cell mediated autoimmune diseases like myasthenia gravis, Morbus Basedow, Hashimoto thyroiditis or Goodpasture syndrome or
                                                                                                                    bscCD19xCD3 antibody; bispecific single-chain fragment; CD19 antigen; CD3 antigen; CD19-positive target cell; T-cell stimulation; cytocoxic T-lymphocyte; B-cell maligancy; mysethenia gravis; B-cell mediated autoimmune disease; Morbus Basedow; Hashimoto, thyroiditis; Goodpasture syndrome; B-cell depletion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multifunctional polypeptide for treating B-cell malignancies
                                                                                                                                                                                       non-Hodgkin lymphoma; gene therapy; cancer; viral disease; ds
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14.tag= a /*tag= a/product= "bscCD19xCD3 antibody"
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                         AAZ30332 standard; cDNA; 1611 BP
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1586. .1603
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P-PSDB; AAY43749.
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for the depletion of B- cells and more particularly non-Hodgkin lymphoma in mammals preferably human. They can also delay the pathological conditions caused by these diseases, and can be used for detecting these diseases. The polymorleotide is used for gene therapy. The polypeptides are also used for identifying compounds modulating B-cell/T-cell mediated immune response with can in turn be used for treating cancer, its related diseases and also for inhibiting viral diseases by preventing viral
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Pred. No. 3.7e-93;
0; Mismatches 158;
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Best Local Similarity 73.5%;
Matches 564; Conservative
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Search completed: April 26, 2004, 16:01:08 Job time : 399 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model	April 26, 2004, 15:43:37 ; Search time 3232 Seconds (without alignments) 9937.249 Million cell updates/sec	US-10-620-049-24 score: 741 : gatattcagatgacacagaccctcagtcaccgtctcctcg 741	table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	: 3470272 segs. 21671516995 regidues
OM nucleic - nuc	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000

6940544

Total number of hits satisfying chosen parameters:

em htg hum: *
em htg inv: *
em htg other: *
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em htg rod: * em_ro:* em_sts:* em_un:* GenEmbl:* Database :

Pred. No. is the number of results predicted by chance to have a

em_htgo_mus:* em_htgo_other:*

htgo_hum:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	קרומקע דווומקע		م و رو				
		Score	Match	Length	BB :	QI	Description
	т	. 66	~	180	ω	BD237850	BD237850 Anti-CD3
	7	99.	67.	1940	ø	AX306601	AX306601 Sequence
	ო	99	67.	94	o'	AX306600	AX306600 Sequence
	4 t	825	65.	o o	ω v	AX306590	AX306590 Sequence
	n v	, t		7 C	۰ م	AKIIBIUS	TARGOA COMICHED
	9 1	474	64.7	916	שם	145504 AR256099	AR256099 Seguence
	- 00	79.	64	916	9	AR401482	AR401482 Sequence
	თ	56.	61.	74	12	AF536561	AF536561 Synthetic
	10	31.	58.	63	9	AX306662	AX306662 Sequence
	TT.	N 1	56.	n i	9	AX797328	AX797328 Sequence
	12	47	56.	g,	y v	AX797327	AX797327 Sequence
	13	٠. د	, d	1457	ρV	E3546U 343682F8	AY3087EB Semience
	r 40	4 4	. 4	100	o w	AX011206	AX011206 Sequence
	10		5.4	60	9	BD206134	BD206134 Polyvalen
	17	5	53	88	12	AF132308	AF132308 Synthetic
,	18	95.	53.	31	ø	AX739885	AX739885 Sequence
	19	•	53	1611	φı	AX014270	AX014270 Sequence
	0 10	4.5		55	۰ م	AX839766	AX839766 Sequence
	7 6	υ 4, υ	, ,	⊣ 6	٠, ٩	BD205046	1140932 Simthetic e
	N (C)	ຸດຕ	י ה מי	2 6	4 6	• -	Sequence
	24	9	52	1637	ø	BD222155	BD222155 Immunolog
	25	•	51.	8	ų	A18692	A18692 Synthetic n
	56	74	20.	1817	9	AX739887	AX739887 Sequence
	22	77	50.	5	ψı	AX057943	AX057943 Sequence
	20.00	øι	4, . O C	786	۰ م	AX/98501	AX/98501 Sequence
	27 C	o١	4, 4 20 0	9,5	۰ م	AX798489	AX798489 Sequence
	ט גי	מיני	4, 4 V Q	7 6	ט ע	AX/384/9 AX/03363	AX/364/9 Sequence
	. W		4, 4,	2871	o w	BD222937	BD222937 Heteromin
	33	61.	48.	65	9	AX011208	AX011208 Sequence
	34	61.	48.	65	ø	BD206135	BD206135 Polyvalen
	35	58.	48.	877	9	E31225	E31225 Device for
	36	58.	48	925	φ		tibody an
	37	9	84.	84	17	AF329458	AF329458 Synthetic
	מ מית	ου ου	4, 2 20 0	אנ	۷ م	AK06067/	ARU60677 Sequence
	υ 4 υ ⊂	מים	τ, Δ ο α	7 6	ρų	AK0/4434 AD060674	ARO/4434 SEQUEICE
	4. 4.	5 6		1 (1	o w	AR074431	AR074431 Sequence
	4 2	50		12	v	AR060673	AR060673 Sequence
	4.3	356.4	ω.	6727	v	AR074430	AR074430 Sequence
	44	ū	æ,	79	9	AR060676	AR060676 Sequence
	45	ū	œ.	7.9	9	AR074433	AR074433 Sequence
						ALIGNMENTS	
	RESULT 1						
	BD237850 LOCUS		BD237850			1803 bp DNA	linear PAT 17-JUL-2003
	FETNIEGO	140		40000		1,000	3

BD237850 1803 bp DNA linear PAT Anti-CD3 immunotoxins and therapeutic uses therefor. BD237850.1 GI:33047620 BD237850.1 GI:3002787850.1 GI:300278787850.1 G LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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1247
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          1308 GAIGGAACTGTTAAACTCCTGATCTACACATCAAGATTACACTCAGGAGTCCCATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neville, D.M., Thompson, J.T., Hu, H., Woo, J.H., Ma, S., and Digan, M.E.
Immunotoxin fusion proteins and means for expression Patent: WO 0187982-A 41 22-NOV-2001,
THE DEPARTMENT OF HEALTH & HUMAN SERVICES (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                         linear
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/organism="synthetic construct"
/molltype="unassigned DNA"
/db_xref="taxon:32630"
/noTe="/Note = synthetic construct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.4%; Score 499.4; DB 6; 81.4%; Pred. No. 2.2e-136;
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                                                                                                                                                                                                                                                                         DNA
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Sequence 41 from Patent W00187982.
AX306601
                                                                                                                  GGCGCAGGGACCACGGTCACCGTCTCCTC
                                                                                          712 GGTCAAGGAACCTCAGTCACCGTCTCCTC
                                                                                                                                                                                                                                                                                                                                                AX306601.1 GI:17645800
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artificial sequences.
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Matches 610;
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VERSION
KEYWORDS
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AUTHORS
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OS Artificial Sequence
PN JP 200253441-A/1
PD 15-OCT-2002
PF 13-JAN-2000 JP 2000593098
PR 15-JAN-2000 JP 2000593098
PR 15-JAN-1999 US 09/23245,25-JAN-1999 US 09/236968 PR 07-OCT-1999 US 09/413134
PI MARY ELLEN DIGAN.PHILIP LAKE,RICHARD MICHAEL WRIGHT PC A61K39/395,A61K31/327,A61K31/343,A61K31/42,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52,A61K31/52
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.2e-136;
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    1803
    Oorganism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"

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1602 AAGCCTGGAGCTTCAATGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTAC 1661
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Immunotoxin fusion proteins and means for expression thereof Patent: WO 0187982-A 30 22-NOV-2001;
THE DEPARTMENT OF HEALTH & HUMAN SERVICES (US)
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                                                                                                                                                                                                                                                                          1782 GACAAGTCATCCAGCACAGCCTACATGGAACTCCTCAGTCTGACATCTGAGGACTCTGCA
                                                                                                                                                                                                                                                                                                                   661 GTCTATTTCTGTGCAAGATCGGGGTTGCTACGTTATGCT-----ATGGACTACTGG
                                                                                                       1662 ACCATGAACTGGGTGAAGCAGAGTCATGGAAAGAACCTTGAGTGGATGGGACTTATTAAT
                                                                                                                                                                                                                                  GACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACCTCTGTGGACTCTGCGC
                                                                    481 TGGATGAACTGGGTGAAGCAGAGGCCTGGACAGGGTCTTGAGTGGATTGGACGGATTTAT
                                                                                                                                                   CCTGGAGATGGAGATTCTAACTACAATGGGAAATTCGAGGGCAAAGGCCATACTGACAGCA
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:33630"
/noTe="/Note = synthetic construct"
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                                                                                                                                                                                                                                                                                                                                                                                                                        1902 GGCGCAGGGACCACGGTCACCGTCTCCTC 1930
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Sequence 30 from Patent WO0187982.
AX306590.
AX306590.1 GI:17645796
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      1719 CCTTACAAAGGTGTTAGTACCTACAACCAGAAGTTCAAGGACAAGGCCACATTAACTGTA 1778
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                                                                                                                                                                                                                                                                                                                                                                                 PAT 11-DEC-2001
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                                                                                                                                                   711
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Immunotoxin fusion proteins and means for expression thereof
Patent: WO 0197982-A 40 22-NOV-2001;
THB DEPARTWENT OF HEALTH & HUMAN SERVICES (US)
Location/Qualifiers
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                                                                                                     1779 GACAAGTCATCCAGCACAGCCTACATGGAACTCCTCAGTCTGACATCTGAGGACTCTGCA
                                                                      GACAAATCCTCCAGCACACACCTACATGCAGCTCAGCAGCCTGACCTCTGTGGACTCTGCG
                                                                                                                                                   GICTATITICIGIGGAAGATCGGGGTTGCTACGTTATGCT-----ATGGACTACTGG
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/organism="synthetic construct"
/mo! Lype="tunasaigned DNA"
/db_xref="taxon:32630"
/note="/Note = synthetic construct"
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Sequence 40 from Patent WC0187982.
AX306600
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Ledbetter, J.A., Gilliland, L.K., Hayden, M.S., Linsley, P.S.,
Bajorath, J. and Fell, H.Perry.
Bajorath, J. and Fell, H.Perry.
Brythession vectors encoding bispecific fusion proteins and methods of producing biologically active bispecific fusion proteins in a mammalian cell
Patent: US 5637481-A 29 10-JUN-1997;
Location/Qualifiers
1. 916
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                                                                                                                                                                         GGCACCAAGCTGGAAATAAAACGTGGTGGTGGTTCTGATGGTGGTTGTTCTGGCGGC 360
     256 AGGITCAGIGGCAGIGGGICIGGAACAGAITAITCICICACCATIGCCAACCIGCAACCA 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u> AAGCCTGGAGCTTCAATGACAATGTCCTGCAAGGCCTCTGGTTACTCATTCACTGGCTAC</u>
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                                                                                                                   316 GAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTGGACGTTCGGTGGA
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Pred. No. 2e-130;
0; Mismatches 148;
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Sequence 29 from patent US 5637481.
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/mol_type="unassigned DNA"
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Ledbetrer, J. A., Gilliland, L.K., Hayden, M.S., Linsley, P.S.,
Ledbetrer, J. A., Gilliland, L.K., Hayden, M.S., Linsley, P.S.,
Bajorath, J. and Fell, H. Perry.
Expression vectors encoding bispecific fusion proteins and mammalian cell
mammalian cell
Patent: US 6132992-A 29 17-0CT-2000;
Location/Qualifiers
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/organism="unknown"
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Sequence 29 from patent US 6132992.
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AR116105.1 GI:14096427
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Unknown.
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I (bases 1 to 916)

Expression vectors encoding bispecific fusion proteins and methods of producing biologically active bispecific fusion proteins in a mammalian cell

Patent: US 6623940-A 29 23-SEP-2003;

Location/Qualifiers

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Sequence 29 from patent US 6623940.
AR401482.1 GI:40148818
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1 (bases 1 to 916)
Ledbetter, J.A., Hayden, M.S., Linsley, P.S., Bajorath, J., Fell, H.P.
Ledbetter, J.A., Hayden, M.S., Linsley, P.S., Bajorath, J., Fell, H.P.
Expression vectors encoding bispecific fusion proteins and methods of producing biologically active bispecific fusion proteins in a mammalian cell
Patent: US 6482919-A 29 19-NOV-2002;
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Sabarth, N., Bumann, D. and Meyer, T.F.
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                                                                                                                                                                                                                                                                                                                      181 AGGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCCCTCACCATTAACAACCTGGAGCAG
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                                                                                       Gaps
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m
                                                  Length 916;
                                                                                       Indels
                                             Score 479.2; DB 6;
Pred. No. 2e-130;
0; Mismatches 148;
                                                                                                                                 GATATTCAGATGACACAGACTACATCCTCCCTGTCTGCCT
                                                  64.78;
79.48;
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                                                Query Match
Best Local Similarity 79.4
Matches 581; Conservative
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/note="reacts with Helicobacter pylori surface protein"
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/transl_table=11
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SAVYYCALLGNNYGYPDVWGAGTSVTVSSAS"
Unpublished
2 (bases 1 to 748)
2 sabarth,N. Bumann,D. and Meyer,T.F.
Subarth,N. Bumann,D. and Meyer,T.F.
Direct Submission
Submitted (08-AUG-2002) Molecular Biology, Max-Planck-Institute for Submitted (08-AUG-2002) Molecular Biology, Schuhmanstr. 20/21, Berlin 10117, Germany Infection Biology, Schuhmanstr. 20/21, Berlin 10117, Germany
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCAGTTGCAGGCAAGTCAGGACATTAGGAATTATTTAAACTGGTATCAGCAGAAACCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                         1. .748
/organism="synthetic construct"
/mol_type="mRNA"
/isolation_source="Mus musculus BALB/c"/db_xref="taxon:32630"
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1. 1953
1. 1953
1. The second construct and type "wassigned DNA"

/mol type "taxon:32630"

/note="nucleic acid sequence coding for fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 GATATCCAGATGACACAGACTACATCCTCCCTCTGCCTCTCTGGGAGACAGAGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GTCAGTTGCAGGCAAGTCAGGACATTAGGAATTATTTAAACTGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GACGGAACTGTTAAATTCCTGATCTACTACACATCAAGATTACTGCCAGGAGTCCCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGTTCAGTGGCAGTCTGGAACAGATTATTCCCTCACCATTAACAACCTGGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 AGGITCAGIGGCAGIGGGICTGGGACAGAIIAIICICICAGCAICAGCAACCIGGAACCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGCCTGGGGCCTCAGTGAAGATTTCCTGCAAAGATTCTGGCTACGCATTCAATAGCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 GGCGGCTCCCGGTGGTGGTGGATCCGAGGTCCAACTGCAACAGTCTGGACCTGAGCTGGTG
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                                cerracaaggereregaceracaaceagagricaaggacaaaggeeracereera
                                                                                                  1762 GACAAGTCATCCAGCACAGCCTACATGGAACTCCTCAGTCTGACATCTGAGGACTCTGCA
                                                                                                                                    GTCTATTTCTGTGCAAGATCGGGGTTGCTACGTTATGCT-----ATGGACTACTGG
                                                                   GACAAATCCTCCAGCACACCCTACATGCAGCTCAGCAGCCTGACCTCTGTGGACTCTGCG
CCTGGAGATGGAGATTCTAACTACAATGGGAAATTCGAGGGCAAGGCCATACTGACAGC
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9
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Anti-Gay immunocoxin as fusion protein
Patent: WO 2051926-A 5 26-JUN-2003;
Friedrich-Alexander-Universitaet Erlangen-Nuernberg (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1953;
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al Similarity 74.9%; Score 421; DB 6; Length 19
al Similarity 74.9%; Pred. No. 3.7e-113;
555; Conservative 0; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                                                                         GGTGCTGGTACTACTGTCACTGTCTCCTC 1910
                                                                                                                                                                                                     GGTCAAGGAACCTCAGTCACCGTCTCCTC 740
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Sequence 5 from Patent W003051926.
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Immunotoxin fusion proteins and means for expression thereof
Patent: WO 0187982-A 102 22-NOV-2001;
THB DEPARTMENT OF HEALTH & HUMAN SERVICES (US)
Location/Qualifiers
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                  GTCTATTTCTGTGCAAGATCGGGGTTGCTACGTTATGCTATGGACTACTGGGGTCAAGGA
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Pred. No. 2.4e-116;
0; Mismatches 152;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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C12R1:91)
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Pred. No. 1.8e-112;
0; Mismatches 184;
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Hagywara, H., Accisuka, Y. and Miyahara, J.
Method for inducing apoptosis
Patent: JP 2000102389-A 7 11-APR-2000;
YOSHHIDE HAGIWARA, HIDEAKI HAGIWARA
OS Artifical Sequence
PN JP 2000102389-A/7
PD 11-APR-2000
PF 29-SEP-1998 JP 1998291441
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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E35160.1 GI:1862419
JP 2000102389-A/7.
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Anti-cd7 immunocoxin as fusion protein
Patent: WO 0301926-A 4 26-JUN-2003;
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Mus sp.
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Ammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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GTCAGTTGCAGGGCAAGTCAGGACATTAGGAATTATTTAAACTGGTATCAGCAGAAACCA
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Antibody and/or chemokine constructs which bind to receptor and their use in immunological disorders Patent: WO 020615-A 17 14-MAR-2002;
Micromet AG (DE)
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/mol type="unassigned DNA"
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KASGYTFTRYTMHWYKQRPGGGLEWIGYINBSRGYTRYNQKEKDKATLTTDKESSTAY
WOLSGITZBEDSAVYYCHRYDDHYSLDTDYWGGGTTLTVSSAKTTPKLGGDILLTGTPAS
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SYMMWYQQKSGTSFKWIYDTSKLASGVPAHFRGSGSCTSYSLISGMBABDAATYC
QQMSSNPFTFGSGTKLEINRADTAPTGSEQKLISEBELNSHHHHH"
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              PAT 06-SEP-2000
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                                                                                                                                                            Kipriyanov, S. and Little, M.
Multivalent antibody constructs
Patent: WO 9957150-A 1 11-NOV-1999;
DEUTSCHES KREBSFORSCH (DE); KIPRIYANOV SERGEJ (DE); LITTLE MELVYN (DE)
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54.5%; Score 404.2; DB 6; Length 1698;
Best Local Similarity 73.5%; Pred. No. 3.4e-108;
Matches 577; Conservative 0; Mismatches 163; Indels 45; Gaps
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'db xref="GI:9997787"

'db_xref="REMTREMBL:CAC07542"
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                                                                                                                                                                                                                                                                                                /mol_type="unassigned DNA"
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451 AAAGATTCTGGCTACGCATTCAATAGCTCTTGGATGAACTGGGTGAAGCAGAGGCCTGGA
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